



## SEQUENCE LISTING

<110> KAO CORPORATION  
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Takimura, Yasushi  
Sato, Tsuyoshi

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<141> 2004-04-09

<150> 2003-106709

<151> 2003-04-10

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<170> PatentIn version 3.2

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Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
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Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	165	170	175	
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Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	195	200	205	
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	210	215	220	
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	225	230	235	240
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	245	250	255	
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Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	275	280	285	
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 Arg Ile His Thr Asn Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr



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Gln 205	Phe	Ser	Ser	Arg	Gly	Pro 210	Thr	Lys	Asp	Gly	Arg 215	Ile	Lys	Pro	Asp	
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340

345

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 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly  
 65 70 75 80  
  
 gca acg aat aaa gga atg gca cct caa gcg aat ctg gtt ttt caa tcc 288

Ala	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	
				85					90					95		
atc	atg	gat	agc	agt	ggg	ggg	ctt	gga	ggc	ttg	cct	tcc	aat	ctg	caa	336
Ile	Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln	
			100					105					110			
acc	tta	ttc	agc	caa	gca	ttc	agt	gca	ggg	gcc	aga	att	cat	aca	aac	384
Thr	Leu	Phe	Ser	Gln	Ala	Phe	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	
		115					120					125				
tcc	tgg	ggg	gca	gcg	gtg	aat	ggg	gcc	tac	acg	aca	gat	tcc	aga	aat	432
Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn	
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gtg	gat	gac	tat	gta	agg	aaa	aat	gat	atg	acg	att	ctt	ttc	gcg	gct	480
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala	
	145				150					155					160	
ggg	aat	gaa	ggg	ccg	aac	ggc	ggg	acc	atc	agt	gca	cct	ggg	acg	gct	528
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	
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aaa	aac	gcc	atc	act	gtc	ggc	gca	acc	gaa	aac	ctg	cgt	cca	agc	ttc	576
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	
			180					185					190			
ggg	tcc	tat	gca	gat	aat	att	aac	cac	gtt	gca	cag	ttc	tct	tcc	cgt	624
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
ggc	ccg	aca	aaa	gat	ggg	cga	atc	aag	cct	gat	gtc	atg	gcg	cca	ggg	672
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
	210					215					220					
aca	tac	att	tta	tca	gca	aga	tct	tct	ctt	gca	ccc	gat	tcc	tcc	ttc	720
Thr	Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
	225				230					235					240	
tgg	gcg	aat	cat	gac	agc	aaa	tat	gcc	tat	atg	ggg	gga	acg	tcc	atg	768
Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
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gca	aca	ccg	att	gtt	gcg	ggg	aat	gtt	gca	cag	ctc	cgt	gag	cat	ttt	816
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
			260					265					270			
gtg	aaa	aat	aga	gga	atc	act	cct	aag	cct	tcc	cta	ttg	aaa	gca	gct	864
Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
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Leu	Ile	Ala	Gly	Ala	Ala	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Asn	Gly	Asn		
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Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr		
305					310					315					320		
gtg	aac	gaa	tcc	agt	gcc	cta	tca	act	agc	caa	aaa	gcg	aca	tat	acc		1008
Val	Asn	Glu	Ser	Ser	Ala	Leu	Ser	Thr	Ser	Gln	Lys	Ala	Thr	Tyr	Thr		
				325					330					335			
ttt	act	gca	acg	gcg	ggc	aag	cca	ttg	aaa	atc	tcc	ctg	gta	tgg	tcg		1056
Phe	Thr	Ala	Thr	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser		
			340					345					350				
gat	gcc	cct	gca	agc	act	act	gct	tct	gta	acc	ctg	gtc	aat	gat	ttg		1104
Asp	Ala	Pro	Ala	Ser	Thr	Thr	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu		
		355					360					365					
gat	ttg	gtc	att	aca	gca	cca	aac	gga	aca	aga	tat	gtc	ggg	aat	gac		1152
Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Arg	Tyr	Val	Gly	Asn	Asp		
	370					375					380						
ttc	tca	gca	cca	ttt	gac	aat	aac	tgg	gat	ggc	cgc	aat	aac	gta	gaa		1200
Phe	Ser	Ala	Pro	Phe	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu		
385					390					395					400		
aat	gta	ttt	att	aat	tcg	ccc	caa	agt	gga	aca	tat	acc	att	gag	gtg		1248
Asn	Val	Phe	Ile	Asn	Ser	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val		
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caa	gca	tat	aat	gtg	ccg	gtt	gga	cca	caa	aac	ttc	tcg	ttg	gca	att		1296
Gln	Ala	Tyr	Asn	Val	Pro	Val	Gly	Pro	Gln	Asn	Phe	Ser	Leu	Ala	Ile		
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gtg	aac																1302
Val	Asn																

<210> 13  
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 <212> PRT  
 <213> Bacillus sp. KSM-kp9860

<400> 13

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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Ile	Val	Ala	Val	Ala	Asp	Thr	Gly		
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	20		25		30												
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly		
	35						40					45					
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp		
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Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly		
65					70					75					80		
Ala	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser		
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Ile	Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Gln		
			100					105					110				
Thr	Leu	Phe	Ser	Gln	Ala	Phe	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn		
		115					120					125					
Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn		
	130					135					140						
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala		
145					150					155					160		
Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala		
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Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe		
			180					185					190				
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg		
		195					200					205					
Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly		
	210					215					220						
Thr	Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe		

225		230		235		240
Trp	Ala	Asn	His	Asp	Ser	Met
				245		255
Ala	Thr	Pro	Ile	Val	Ala	Gln
			260			270
Val	Lys	Asn	Arg	Gly	Ile	Thr
		275			280	285
Leu	Ile	Ala	Gly	Ala	Ala	Asp
	290					295
Gln	Gly	Trp	Gly	Arg	Val	Thr
305					310	315
Val	Asn	Glu	Ser	Ser	Ala	Leu
				325		330
Phe	Thr	Ala	Thr	Ala	Gly	Lys
			340			345
Asp	Ala	Pro	Ala	Ser	Thr	Thr
		355				360
Asp	Leu	Val	Ile	Thr	Ala	Pro
	370					375
Phe	Ser	Ala	Pro	Phe	Asp	Asn
385					390	395
Asn	Val	Phe	Ile	Asn	Ser	Pro
				405		410
Gln	Ala	Tyr	Asn	Val	Pro	Val
			420			425
Val	Asn					



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 <212> DNA  
 <213> Bacillus sp. KSM-9865

<220>  
 <221> CDS  
 <222> (1)..(1302)  
 <223> Protease 9865

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 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Ser Ser  
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 tac ggg ttg tat gga caa gga cag atc gta gcg gtt gcc gat aca ggg 96  
 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly  
 20 25 30  
 ctt gat aca ggt cgc aat gac agt tcg atg cat gaa gcc ttc cgg ggg 144  
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
 35 40 45  
 aaa att act gca tta tat gca ttg gga cgg acg aat aat gcc aat gat 192  
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
 50 55 60  
 acg aat ggt cat ggt acg cat gtg gct ggc tcc gta tta gga aac ggc 240  
 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly  
 65 70 75 80  
 tcc act aat aaa gga atg gcg cct cag gcg aat cta gtc ttc caa tct 288  
 Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser  
 85 90 95  
 atc atg gat agc ggt ggg gga ctt gga gga cta cct tcg aat ctg caa 336  
 Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln  
 100 105 110  
 acc tta ttc agc caa gca tac agt gct ggt gcc aga att cat aca aac 384  
 Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn  
 115 120 125  
 tcc tgg gga gca gca gtg aat ggg gct tac aca aca gat tcc aga aat 432  
 Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
 130 135 140  
 gtg gat gac tat gtg cgc aaa aat gat atg acg atc ctt ttc gct gcc 480

Val 145	Asp	Asp	Tyr	Val	Arg 150	Lys	Asn	Asp	Met	Thr 155	Ile	Leu	Phe	Ala	Ala 160	
ggg Gly	aat Asn	gaa Glu	gga Gly	ccg Pro 165	aac Asn	ggc Gly	gga Gly	acc Thr	atc Ile 170	agt Ser	gca Ala	cca Pro	ggc Gly 175	aca Thr	gct Ala	528
aaa Lys	aat Asn	gca Ala	ata Ile 180	aca Thr	gtc Val	gga Gly	gct Ala	acg Thr 185	gaa Glu	aac Asn	ctc Leu	cgc Arg	cca Pro 190	agc Ser	ttc Phe	576
ggg Gly	tct Ser	tat Tyr 195	gcg Ala	gac Asp	aat Asn	atc Ile	aac Asn 200	cat His	gtg Val	gca Ala	cag Gln	ttc Phe 205	tct Ser	tca Ser	cgt Arg	624
gga Gly	ccg Pro 210	aca Thr	aag Lys	gat Asp	gga Gly	cgg Arg 215	atc Ile	aaa Lys	ccg Pro	gat Asp	gtc Val 220	atg Met	gca Ala	ccg Pro	gga Gly	672
acg Thr 225	ttc Phe	ata Ile	cta Leu	tca Ser	gca Ala 230	aga Arg	tct Ser	tct Ser	ctt Leu	gca Ala 235	ccg Pro	gat Asp	tcc Ser	tcc Ser	ttc Phe 240	720
tgg Trp	gcg Ala	aac Asn	cat His 245	gac Asp	agt Ser	aaa Lys	tat Tyr	gca Ala	tac Tyr 250	atg Met	ggg Gly	gga Gly	acg Thr 255	tcc Ser	atg Met	768
gct Ala	aca Thr	ccg Pro	atc Ile 260	gtt Val	gct Ala	gga Gly	aac Asn 265	gtg Val	gca Ala	cag Gln	ctt Leu	cgt Arg	gag Glu 270	cat His	ttt Phe	816
gtg Val	aaa Lys 275	aac Asn	aga Arg	ggc Gly	atc Ile	aca Thr	cca Pro 280	aag Lys	cct Pro	tct Ser	cta Leu	tta Leu 285	aaa Lys	gcg Ala	gca Ala	864
ctg Leu 290	att Ile	gcc Ala	ggg Gly	gca Ala	gca Ala	gac Asp 295	atc Ile	ggc Gly	ctt Leu	ggc Gly	tac Tyr 300	ccg Pro	aac Asn	ggg Gly	aac Asn	912
caa Gln 305	gga Gly	tgg Trp	gga Gly	cga Arg	gtg Val 310	aca Thr	ttg Leu	gat Asp	aaa Lys 315	tcc Ser	cta Leu	aac Asn	gtt Val	gcc Ala	tat Tyr 320	960
gtg Val	aac Asn	gag Glu	tcc Ser	agt Ser 325	tct Ser	cta Leu	tcc Ser	acc Thr	agc Ser 330	caa Gln	aaa Lys	gcg Ala	acg Thr 335	tac Tyr	tcg Ser	1008
ttt Phe	act Thr	gct Ala	act Thr 340	gcc Ala	ggc Gly	aag Lys	cct Pro 345	ttg Leu	aag Lys	atc Ile	tcc Ser	ctg Leu	gta Val 350	tgg Trp	tct Ser	1056
gat	gcc	cct	gcg	agc	aca	act	gct	tcc	gta	acg	ctt	gtc	aat	gac	ctg	1104

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Asp	Ala	Pro	Ala	Ser	Thr	Thr	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu	
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gac	ctt	gtc	att	acc	gct	cca	aat	ggc	aca	caa	tat	gtt	gga	aat	gac	1152
Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Gln	Tyr	Val	Gly	Asn	Asp	
	370					375					380					
ttt	act	tcg	cca	tac	aat	aat	aac	tgg	gat	ggc	cgc	aat	aac	gta	gaa	1200
Phe	Thr	Ser	Pro	Tyr	Asn	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	
	385				390					395					400	
aat	gta	ttt	att	aat	gcg	cca	caa	agc	ggg	acg	tat	aca	att	gag	gta	1248
Asn	Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	
				405					410					415		
cag	gct	tat	aac	gta	ccg	gtt	gga	cca	cag	acc	ttc	tcg	ttg	gca	att	1296
Gln	Ala	Tyr	Asn	Val	Pro	Val	Gly	Pro	Gln	Thr	Phe	Ser	Leu	Ala	Ile	
			420					425					430			
gtg	aac															1302
Val	Asn															

<210> 15  
 <211> 434  
 <212> PRT  
 <213> Bacillus sp. KSM-9865

<400> 15

Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Ser	Ser	
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Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Ile	Val	Ala	Val	Ala	Asp	Thr	Gly	
			20					25					30			
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				
Lys	Ile	Thr	Ala	Leu	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
	50					55					60					
Thr	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly	
	65				70					75					80	
Ser	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	

85

90

95

Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln  
 100 105 110

Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn  
 115 120 125

Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
 130 135 140

Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala  
 145 150 155 160

Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
 165 170 175

Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
 180 185 190

Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
 195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
 210 215 220

Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
 225 230 235 240

Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
 245 250 255

Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
 260 265 270

Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
 275 280 285

Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn

290

295

300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr  
 305 310 315 320

Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser  
 325 330 335

Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
 340 345 350

Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu  
 355 360 365

Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp  
 370 375 380

Phe Thr Ser Pro Tyr Asn Asn Asn Trp Asp Gly Arg Asn Asn Val Glu  
 385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val  
 405 410 415

Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr Phe Ser Leu Ala Ile  
 420 425 430

Val Asn

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 <211> 1299  
 <212> DNA  
 <213> Bacillus sp. D-6

<220>  
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 <222> (1)..(1299)  
 <223> Protease E-1

<400> 16  
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48

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tta Leu	gat Asp	aca Thr 35	ggt Gly	cgt Arg	aac Asn	gat Asp	agt Ser 40	tct Ser	atg Met	cat His	gaa Glu	gca Ala 45	ttc Phe	cgt Arg	ggg Gly	144
aaa Lys	att Ile 50	aca Thr	gct Ala	ctt Leu	tac Tyr	gcg Ala 55	tta Leu	gga Gly	aga Arg	act Thr	aac Asn 60	aat Asn	gca Ala	aat Asn	gat Asp	192
ccg Pro 65	aat Asn	ggg Gly	cat His	ggt Gly 70	acg Thr	cat His	gta Val	gct Ala	ggt Gly 75	tct Ser	gtg Val	ctt Leu	ggt Gly	aat Asn	gct Ala 80	240
tta Leu	aat Asn	aaa Lys	gga Gly 85	atg Met	gct Ala	ccg Pro	caa Gln	gct Ala	aac Asn 90	tta Leu	gtc Val	ttc Phe	caa Gln	tct Ser 95	att Ile	288
atg Met	gat Asp	agc Ser	agc Ser 100	gga Gly	gga Gly	tta Leu	gga Gly	gga Gly 105	tta Leu	cca Pro	tcg Ser	aat Asn	tta Leu 110	aat Asn	acg Thr	336
tta Leu	ttt Phe 115	agt Ser	caa Gln	gct Ala	tgg Trp	aat Asn	gct Ala 120	ggc Gly	gct Ala	aga Arg	att Ile 125	cat His	act Thr	aac Asn	tct Ser	384
tgg Trp 130	ggg Gly	gcc Ala	cca Pro	gta Val	aat Asn	gga Gly 135	gcg Ala	tac Tyr	act Thr	gct Ala	aac Asn 140	tcg Ser	aga Arg	caa Gln	gtg Val	432
gat Asp 145	gag Glu	tat Tyr	gtt Val	cga Arg	aac Asn 150	aat Asn	gat Asp	atg Met	acg Thr 155	gta Val	ctt Leu	ttt Phe	gca Ala	gct Ala	gga Gly 160	480
aat Asn	gaa Glu	gga Gly	cct Pro	aac Asn 165	tct Ser	gga Gly	aca Thr	att Ile	agc Ser 170	gct Ala	cca Pro	ggg Gly	aca Thr 175	gcg Ala	aaa Lys	528
aat Asn	gcc Ala	att Ile	acg Thr 180	gtc Val	ggc Gly	gca Ala	acg Thr	gaa Glu 185	aac Asn	tac Tyr	cga Arg	cca Pro	agt Ser 190	ttt Phe	ggt Gly	576
tca Ser	att Ile 195	gca Ala	gat Asp	aac Asn	cct Pro	aat Asn	cat His 200	atc Ile	gca Ala	caa Gln	ttt Phe 205	tca Ser	tcg Ser	aga Arg	gga Gly	624
gct	acg	aga	gat	gga	cga	att	aaa	cca	gac	gta	aca	gct	cct	gga	aca	672

Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr	
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ttt	ata	tta	tca	gca	cgc	tct	tct	tta	gca	cca	gac	tct	tcg	ttt	tgg	720
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	
225					230					235					240	
gcg	aat	tat	aac	agt	aag	tat	gcg	tat	atg	ggc	ggt	acc	tct	atg	gcg	768
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	
				245					250					255		
aca	cct	ata	gtt	gcg	ggg	aat	gtc	gcg	caa	tta	cgc	gag	cat	ttt	ata	816
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile	
			260					265					270			
aaa	aat	aga	gga	att	aca	cct	aaa	cct	tcc	tta	ata	aaa	gct	gca	ctt	864
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu	
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Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln	
	290					295					300					
ggc	tgg	ggg	cgt	gtt	act	tta	gat	aaa	tcg	tta	aat	gta	gcg	tat	gtc	960
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val	
305					310					315					320	
aat	gaa	gca	act	gca	tta	aca	aca	gga	caa	aaa	gca	acg	tat	tcg	ttc	1008
Asn	Glu	Ala	Thr	Ala	Leu	Thr	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe	
				325					330					335		
caa	acg	caa	gcg	ggg	aaa	cca	tta	aaa	atc	tcg	tta	gta	tgg	aca	gat	1056
Gln	Thr	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp	
			340					345					350			
gca	cct	gga	agt	aca	aca	gca	tct	tat	aca	cta	gtt	aat	gat	tta	gat	1104
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp	
		355					360					365				
cta	gtt	att	act	gct	ccg	aat	gga	caa	aaa	tat	gta	ggg	aat	gat	ttt	1152
Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Gln	Lys	Tyr	Val	Gly	Asn	Asp	Phe	
	370					375					380					
agt	tat	cct	tat	gat	aat	aat	tgg	gat	ggg	cgc	aac	aat	gtt	gag	aac	1200
Ser	Tyr	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	Asn	
385					390					395					400	
gta	ttt	ata	aac	gct	ccg	caa	tct	gga	acg	tat	aca	att	gag	gtt	caa	1248
Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Ile	Glu	Val	Gln	
				405					410					415		
gcg	tat	aac	gtt	cca	tct	gga	cca	cag	cgt	ttc	tca	cta	gct	atc	gta	1296

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

cat  
 His

1299

<210> 17  
 <211> 433  
 <212> PRT  
 <213> Bacillus sp. D-6, Protease E-1

<400> 17

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn  
 1 5 10 15

Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly  
 20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
 35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
 50 55 60

Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala  
 65 70 75 80

Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
 85 90 95

Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
 100 105 110

Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
 115 120 125

Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val  
 130 135 140

Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly



145		150		155		160									
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys
				165					170					175	
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly
			180					185					190		
Ser	Ile	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly
		195					200					205			
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr
	210					215					220				
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp
225					230					235					240
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala
				245					250					255	
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile
			260					265					270		
Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Ile	Lys	Ala	Ala	Leu
		275					280					285			
Ile	Ala	Gly	Ala	Thr	Asp	Val	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asp	Gln
	290					295					300				
Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Tyr	Val
305					310					315					320
Asn	Glu	Ala	Thr	Ala	Leu	Thr	Thr	Gly	Gln	Lys	Ala	Thr	Tyr	Ser	Phe
				325					330					335	
Gln	Thr	Gln	Ala	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Thr	Asp
			340					345					350		
Ala	Pro	Gly	Ser	Thr	Thr	Ala	Ser	Tyr	Thr	Leu	Val	Asn	Asp	Leu	Asp

355

360

365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

His

<210> 18  
 <211> 1299  
 <212> DNA  
 <213> Bacillus sp. Y

<220>  
 <221> CDS  
 <222> (1)..(1299)  
 <223> Gene name Ya,

Protease Ya

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 Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn  
 1 5 10 15  
 tac gga tta tat gga caa ggt caa gta gtt gca gta gcg gac aca ggc 96  
 Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly  
 20 25 30  
 tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgc ggg 144  
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
 35 40 45  
 aaa atc aca gct ctt tac gcg tta gga aga act aat aat gcg agt gat 192  
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp  
 50 55 60

ccg Pro 65	aat Asn	ggg Gly	cat His	ggc Gly 70	aca Thr	cat His	gta Val	gca Ala	ggg Gly 75	tct Ser	gta Val	ctt Leu	ggg Gly	aat Asn 80	gct Ala	240
tta Leu	aat Asn	aaa Lys	gga Gly 85	atg Met	gct Ala	ccg Pro	caa Gln	gct Ala	aac Asn 90	tta Leu	gtc Val	ttc Phe	caa Gln	tct Ser 95	att Ile	288
atg Met	gat Asp	agc Ser 100	agc Ser	gga Gly	gga Gly	tta Leu	ggg Gly 105	ggc Gly	tta Leu	cca Pro	tcg Ser	aac Asn 110	tta Leu	aat Asn	acg Thr	336
tta Leu	ttt Phe 115	agt Ser	caa Gln	gct Ala	tgg Trp	aat Asn 120	gct Ala	gga Gly	gca Ala	aga Arg	att Ile 125	cat His	act Thr	aac Asn	tct Ser	384
tgg Trp 130	gga Gly	gcc Ala	cca Pro	gta Val	aat Asn	gga Gly 135	gcg Ala	tac Tyr	act Thr	gct Ala 140	aac Asn	tcg Ser	aga Arg	caa Gln	gtg Val	432
gat Asp 145	gaa Glu	tat Tyr	gtt Val	cga Arg 150	aat Asn	aat Asn	gat Asp	atg Met	acg Thr 155	gta Val	ctt Leu	ttt Phe	gca Ala	gct Ala	ggg Gly 160	480
aat Asn	gaa Glu	ggg Gly	cct Pro 165	aat Asn	tca Ser	gga Gly	aca Thr	att Ile 170	agt Ser	gct Ala	cca Pro	ggg Gly	aca Thr 175	gcg Ala	aaa Lys	528
aat Asn	gct Ala	att Ile 180	acg Thr	gtc Val	ggc Gly	gca Ala	acg Thr 185	gaa Glu	aac Asn	tat Tyr	cgc Arg	cca Pro	agc Ser 190	ttc Phe	ggg Gly	576
tcg Ser	ata Ile 195	gca Ala	gat Asp	aac Asn	cca Pro	aat Asn	cat His 200	att Ile	gca Ala	caa Gln	ttt Phe 205	tca Ser	tcg Ser	aga Arg	gga Gly	624
gct Ala 210	acg Thr	agg Arg	gat Asp	gga Gly	cga Arg	att Ile 215	aag Lys	cct Pro	gac Asp	gta Val	aca Thr 220	gct Ala	cct Pro	gga Gly	aca Thr	672
ttt Phe 225	att Ile	tta Leu	tca Ser	gca Ala	cgt Arg 230	tct Ser	tcc Ser	tta Leu	gct Ala 235	cca Pro	gac Asp	tct Ser	tcg Ser	ttt Phe	tgg Trp 240	720
gcg Ala	aat Asn	tat Tyr	aac Asn	agt Ser 245	aaa Lys	tac Tyr	gcg Ala	tat Tyr	atg Met 250	ggc Gly	ggg Gly	acc Thr	tcc Ser	atg Met 255	gcg Ala	768
aca Thr	cct Pro	att Ile 260	gtt Val	gca Ala	ggg Gly	aat Asn	gtc Val	gcg Ala 265	caa Gln	tta Leu	cgt Arg	gag Glu	cat His 270	ttt Phe	ata Ile	816

aaa aat aga ggt att act cct aag cct tct tta ata aaa gct gca ctt	864
Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu	
275 280 285	
atc gct ggt gct act gat gtt ggt tta gga tat cct aat ggt gac caa	912
Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln	
290 295 300	
ggc tgg ggg cgt gtt act cta aat aaa tcg tta aat gta gcg tat gtc	960
Gly Trp Gly Arg Val Thr Leu Asn Lys Ser Leu Asn Val Ala Tyr Val	
305 310 315 320	
aat gaa gca act gca tta gcc aca gga caa aaa gca acg tat tcg ttc	1008
Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe	
325 330 335	
caa gca caa gcg ggt aaa cct tta aaa atc tcg tta gta tgg aca gat	1056
Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp	
340 345 350	
gct cct gga agt aca act gca tct tat aca cta gtt aat gat tta gat	1104
Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp	
355 360 365	
cta gtt att act gct ccg aat gga caa aaa tat gta gga aat gat ttt	1152
Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe	
370 375 380	
agt tat cct tat gat aat aac tgg gat ggt cgc aac aat gtt gag aac	1200
Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn	
385 390 395 400	
gta ttt ata aac gct ccg caa tct gga acg tat ata att gag gtt caa	1248
Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln	
405 410 415	
gcg tat aat gta cca tct ggc cca cag cgt ttc tca cta gct atc gta	1296
Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val	
420 425 430	
cat	1299
His	

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 <211> 433  
 <212> PRT  
 <213> Bacillus sp. Y  
  
 <400> 19

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn  
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 Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly  
 20 25 30  
 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
 35 40 45  
 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp  
 50 55 60  
 Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala  
 65 70 75 80  
 Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
 85 90 95  
 Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
 100 105 110  
 Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
 115 120 125  
 Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val  
 130 135 140  
 Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly  
 145 150 155 160  
 Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys  
 165 170 175  
 Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly  
 180 185 190  
 Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly  
 195 200 205

Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr  
 210 215 220

Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp  
 225 230 235 240

Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala  
 245 250 255

Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile  
 260 265 270

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu  
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Asn Gly Asp Gln  
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asn Lys Ser Leu Asn Val Ala Tyr Val  
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp  
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp  
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Ile Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
420 425 430

His

<210> 20  
<211> 1299  
<212> DNA  
<213> Bacillus SD521

<220>  
<221> CDS  
<222> (1)..(1299)  
<223> Gene name SD-521, protease SD521

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Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn  
1 5 10 15  
  
tac gga cta tat gga caa ggt caa gta gtt gca gta gcg gat acg ggt 96  
Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly  
20 25 30  
  
tta gat aca ggt cgt aac gat agt tct atg cat gaa gca ttc cgt ggg 144  
Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly  
35 40 45  
  
aaa att aca gct ctt tac gcg tta gga aga act aac aat gca aat gat 192  
Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
50 55 60  
  
ccg aat ggg cat ggt acg cat gta gca ggt tct gta ctt ggt aat gct 240  
Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala  
65 70 75 80  
  
tta aat aaa gga atg gct ccg caa gct aac tta gtc ttc caa tct att 288  
Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile  
85 90 95  
  
atg gat agc agc gga gga tta ggt gga tta cca tcg aat ttg aat acg 336  
Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr  
100 105 110  
  
tta ttt agt caa gct tgg aat gct ggg gct aga att cat act aac tct 384  
Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser  
115 120 125

tgg Trp	ggt Gly	gct Ala	cca Pro	gta Val	aat Asn	gga Gly	gcg Ala	tac Tyr	act Thr	gct Ala	aac Asn	tcg Ser	aga Arg	caa Gln	gtg Val	432
130						135					140					
gat Asp	gag Glu	tat Tyr	gtt Val	cga Arg	aat Asn	aat Asn	gat Asp	atg Met	acg Thr	gta Val	ctt Leu	ttt Phe	gca Ala	gca Ala	ggt Gly	480
145					150					155					160	
aat Asn	gaa Glu	ggt Gly	cct Pro	aat Asn	tca Ser	gga Gly	aca Thr	att Ile	agt Ser	gct Ala	cca Pro	ggc Gly	aca Thr	gcg Ala	aaa Lys	528
				165					170					175		
aat Asn	gcc Ala	att Ile	acg Thr	gtc Val	ggc Gly	gca Ala	acg Thr	gaa Glu	aac Asn	tat Tyr	cgc Arg	ccg Pro	agc Ser	ttc Phe	ggt Gly	576
			180					185					190			
tca Ser	tta Leu	gca Ala	gat Asp	aac Asn	cca Pro	aat Asn	cat His	atc Ile	gca Ala	caa Gln	ttt Phe	tca Ser	tca Ser	aga Arg	gga Gly	624
		195					200					205				
gct Ala	acg Thr	aga Arg	gat Asp	gga Gly	cga Arg	att Ile	aaa Lys	cca Pro	gac Asp	gta Val	aca Thr	gct Ala	cct Pro	gga Gly	aca Thr	672
	210					215					220					
ttt Phe	att Ile	tta Leu	tca Ser	gca Ala	cgt Arg	tct Ser	tcc Ser	tta Leu	gcc Ala	cca Pro	gac Asp	tct Ser	tcg Ser	ttt Phe	tgg Trp	720
225					230					235					240	
gcg Ala	aat Asn	tat Tyr	aac Asn	agt Ser	aag Lys	tat Tyr	gcg Ala	tac Tyr	atg Met	ggc Gly	ggt Gly	acc Thr	tct Ser	atg Met	gcg Ala	768
				245					250					255		
aca Thr	cct Pro	ata Ile	gtt Val	gcg Ala	ggg Gly	aat Asn	gtc Val	gcg Ala	caa Gln	tta Leu	cgc Arg	gag Glu	cat His	ttt Phe	ata Ile	816
			260					265					270			
aaa Lys	aat Asn	aga Arg	gga Gly	att Ile	aca Thr	cct Pro	aaa Lys	cct Pro	tcc Ser	tta Leu	ata Ile	aaa Lys	gct Ala	gca Ala	ctt Leu	864
		275					280					285				
atc Ile	gct Ala	ggg Gly	gct Ala	act Thr	gat Asp	gtt Val	ggg Gly	tta Leu	gga Gly	tat Tyr	cca Pro	agt Ser	ggg Gly	gac Asp	caa Gln	912
	290					295					300					
ggc Gly	tgg Trp	ggg Gly	cgt Arg	gtt Val	act Thr	cta Leu	gat Asp	aaa Lys	tcg Ser	tta Leu	aat Asn	gta Val	gcg Ala	tat Tyr	gtc Val	960
305					310					315					320	
aat Asn	gaa Glu	gca Ala	act Thr	gca Ala	tta Leu	gca Ala	aca Thr	gga Gly	caa Gln	aaa Lys	gca Ala	acg Thr	tat Tyr	tcg Ser	ttc Phe	1008
				325					330					335		



caa gca caa gcg ggt aaa cct tta aaa atc tcg tta gta tgg aca gat	1056
Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp	
340 345 350	
gca cct gga agt aca act gca tct tat aca cta gtt aat gat tta gat	1104
Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp	
355 360 365	
cta gtt att act gct ccg aat gga caa aaa tat gta gga aat gat ttt	1152
Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe	
370 375 380	
agt tat cct tat gat aat aac tgg gat ggt cgc aac aat gtt gag aac	1200
Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn	
385 390 395 400	
gta ttt ata aac gct ccg caa tct gga acg tat aca att gag gtt caa	1248
Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln	
405 410 415	
gcg tat aat gta cca tct ggc cca cag cgt ttc tca cta gct atc gta	1296
Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val	
420 425 430	
cat	1299
His	

<210> 21  
 <211> 433  
 <212> PRT  
 <213> Bacillus SD521

<400> 21

Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp Val Ala Gln Asn Asn
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Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
20 25 30

Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
35 40 45

Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
50 55 60

Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Ala	65	70	75	80
Leu	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile	85	90	95	
Met	Asp	Ser	Ser	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Leu	Asn	Thr	100	105	110	
Leu	Phe	Ser	Gln	Ala	Trp	Asn	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser	115	120	125	
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Ala	Asn	Ser	Arg	Gln	Val	130	135	140	
Asp	Glu	Tyr	Val	Arg	Asn	Asn	Asp	Met	Thr	Val	Leu	Phe	Ala	Ala	Gly	145	150	155	160
Asn	Glu	Gly	Pro	Asn	Ser	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	Lys	165	170	175	
Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Tyr	Arg	Pro	Ser	Phe	Gly	180	185	190	
Ser	Leu	Ala	Asp	Asn	Pro	Asn	His	Ile	Ala	Gln	Phe	Ser	Ser	Arg	Gly	195	200	205	
Ala	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Thr	Ala	Pro	Gly	Thr	210	215	220	
Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp	225	230	235	240
Ala	Asn	Tyr	Asn	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala	245	250	255	
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Ile	260	265	270	

Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu  
 275 280 285

Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln  
 290 295 300

Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val  
 305 310 315 320

Asn Glu Ala Thr Ala Leu Ala Thr Gly Gln Lys Ala Thr Tyr Ser Phe  
 325 330 335

Gln Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp  
 340 345 350

Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp  
 355 360 365

Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe  
 370 375 380

Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
 385 390 395 400

Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln  
 405 410 415

Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val  
 420 425 430

His

<210> 22  
 <211> 1302  
 <212> DNA  
 <213> NCIB12289

<220>  
 <221> CDS

<222> (1)..(1302)

<223> Gene name A1, protease A1

<400> 22

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Asn	Asp	Val	Ala	Arg	Gly	Ile	Val	Lys	Ala	Asp	Val	Ala	Gln	Ser	Ser	
1				5					10					15		
tat	ggt	tta	tat	ggg	caa	ggg	caa	gtg	gtt	gca	gta	gcg	gat	acc	gga	96
Tyr	Gly	Leu	Tyr	Gly	Gln	Gly	Gln	Val	Val	Ala	Val	Ala	Asp	Thr	Gly	
			20					25					30			
ctg	gat	aca	ggg	cgt	aat	gac	agc	tcg	atg	cat	gaa	gcg	ttc	cga	gga	144
Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly	
		35					40					45				
aag	att	acc	gcg	ata	tat	gcc	ctt	gga	aga	aca	aac	aac	gcc	aat	gat	192
Lys	Ile	Thr	Ala	Ile	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp	
	50					55					60					
cca	aac	gga	cac	ggg	acg	cat	gtt	gcc	gga	tct	gtt	tta	gga	aac	ggt	240
Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly	
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act	tcg	aat	aaa	ggg	atg	gct	cca	caa	gct	aac	tta	gtt	ttc	caa	tct	288
Thr	Ser	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	
				85					90					95		
gtt	atg	gac	agc	aat	ggc	gga	ctt	ggc	gga	ctg	cct	tcc	aat	gta	agt	336
Val	Met	Asp	Ser	Asn	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Val	Ser	
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aca	tta	ttc	agc	cag	gca	tat	agt	gcc	ggt	gcc	aga	atc	cat	acg	aac	384
Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	
		115					120					125				
tca	tgg	gga	gcg	cct	gta	aac	gga	gcg	tac	act	act	gat	tcc	aga	aac	432
Ser	Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn	
	130					135					140					
gta	gac	gat	tat	gtt	cgt	aaa	aat	gat	atg	gcg	gtt	ctt	ttt	gca	gcg	480
Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Ala	Val	Leu	Phe	Ala	Ala	
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Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	Ala	Pro	Gly	Thr	Ala	
				165					170					175		
aag	aat	gct	atc	aca	gta	ggg	gca	aca	gaa	aac	ctg	cgc	cca	agc	ttt	576
Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	Leu	Arg	Pro	Ser	Phe	
			180					185					190			

gga	tct	tat	gct	gac	aac	atc	aat	cat	gta	gca	cag	ttt	tcc	tcc	cgc	624
Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	
		195					200					205				
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Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	
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aca	ttt	att	tta	tcg	gca	aga	tct	tct	ttg	gct	ccg	gac	tcc	tca	ttc	720
Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	
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Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	
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gcg	aca	ccg	att	gta	gct	ggg	aac	gtt	gca	cag	tta	cgt	gaa	cat	ttc	816
Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	
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Ile	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	
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Leu	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Gly	Leu	Gly	Tyr	Pro	Ser	Gly	Asn	
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Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	Leu	Asn	Val	Ala	Phe	
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Val	Asn	Glu	Thr	Ser	Ser	Leu	Ser	Thr	Asn	Gln	Lys	Ala	Thr	Tyr	Ser	
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ttt	act	gca	caa	tca	ggc	aaa	cct	ttg	aag	att	tca	ttg	gtt	tgg	tct	1056
Phe	Thr	Ala	Gln	Ser	Gly	Lys	Pro	Leu	Lys	Ile	Ser	Leu	Val	Trp	Ser	
			340					345					350			
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Asp	Ala	Pro	Ala	Ser	Thr	Ser	Ala	Ser	Val	Thr	Leu	Val	Asn	Asp	Leu	
		355					360					365				
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Asp	Leu	Val	Ile	Thr	Ala	Pro	Asn	Gly	Thr	Lys	Tyr	Val	Gly	Asn	Asp	
	370					375					380					
ttt	act	gct	ccc	tat	gat	aat	aac	tgg	gat	gga	cgt	aac	aat	gta	gag	1200
Phe	Thr	Ala	Pro	Tyr	Asp	Asn	Asn	Trp	Asp	Gly	Arg	Asn	Asn	Val	Glu	
385					390					395					400	

aac	gtg	ttt	atc	aat	gct	ccg	caa	agc	gga	acg	tat	aca	gtt	gag	gta	1248
Asn	Val	Phe	Ile	Asn	Ala	Pro	Gln	Ser	Gly	Thr	Tyr	Thr	Val	Glu	Val	
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cag	gct	tac	aat	gtt	cca	caa	ggg	ccg	cag	gcg	ttt	tct	ttg	gct	att	1296
Gln	Ala	Tyr	Asn	Val	Pro	Gln	Gly	Pro	Gln	Ala	Phe	Ser	Leu	Ala	Ile	
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gtg	aac															1302
Val	Asn															

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Leu	Asp	Thr	Gly	Arg	Asn	Asp	Ser	Ser	Met	His	Glu	Ala	Phe	Arg	Gly
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Lys	Ile	Thr	Ala	Ile	Tyr	Ala	Leu	Gly	Arg	Thr	Asn	Asn	Ala	Asn	Asp
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Pro	Asn	Gly	His	Gly	Thr	His	Val	Ala	Gly	Ser	Val	Leu	Gly	Asn	Gly
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Thr	Ser	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser
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Val	Met	Asp	Ser	Asn	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ser	Asn	Val	Ser
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Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn
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Ser Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn  
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Val Asp Asp Tyr Val Arg Lys Asn Asp Met Ala Val Leu Phe Ala Ala  
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Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala  
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Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe  
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Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg  
 195 200 205

Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly  
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Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe  
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Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met  
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Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe  
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Ile Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala  
 275 280 285

Leu Ile Ala Gly Ala Thr Asp Ile Gly Leu Gly Tyr Pro Ser Gly Asn  
 290 295 300

Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe  
 305 310 315 320

Val Asn Glu Thr Ser Ser Leu Ser Thr Asn Gln Lys Ala Thr Tyr Ser  
 325 330 335

Phe Thr Ala Gln Ser Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser  
340 345 350

Asp Ala Pro Ala Ser Thr Ser Ala Ser Val Thr Leu Val Asn Asp Leu  
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Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp  
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Phe Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu  
385 390 395 400

Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val  
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Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp  
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Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala



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Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	Leu	Val	Phe	Gln	Ser	Ile
				85					90					95	
Met	Asp	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Leu	Pro	Ala	Asn	Leu	Gln	Thr
			100					105					110		
Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	Arg	Ile	His	Thr	Asn	Ser
		115					120					125			
Trp	Gly	Ala	Pro	Val	Asn	Gly	Ala	Tyr	Thr	Thr	Asp	Ser	Arg	Asn	Val
	130					135					140				
Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	Ile	Leu	Phe	Ala	Ala	Gly
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Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	Gln	Phe	Ser	Ser	Arg	Gly
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Pro	Thr	Arg	Asp	Gly	Arg	Ile	Lys	Pro	Asp	Val	Met	Ala	Pro	Gly	Thr
	210					215					220				
Tyr	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	Pro	Asp	Ser	Ser	Phe	Trp
225					230					235					240
Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	Gly	Gly	Thr	Ser	Met	Ala
				245					250					255	
Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	Leu	Arg	Glu	His	Phe	Val
			260					265					270		
Lys	Asn	Arg	Gly	Val	Thr	Pro	Lys	Pro	Ser	Leu	Leu	Lys	Ala	Ala	Leu

275

280

285

Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Phe Pro Asn Gly Asn Gln  
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Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Phe Val  
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Asn Glu Thr Ser Pro Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser Phe  
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Thr Ala Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser Asp  
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Ala Pro Gly Ser Thr Thr Ala Ser Leu Thr Leu Val Asn Asp Leu Asp  
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Leu Val Ile Thr Ala Pro Asn Gly Thr Lys Tyr Val Gly Asn Asp Phe  
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Thr Ala Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn  
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Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Val Glu Val Gln  
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Ala Tyr Asn Val Pro Val Ser Pro Gln Thr Phe Ser Leu Ala Ile Val  
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His